

**Amendments to the Claims:**

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1-13. (Canceled)

14. (Currently Amended) Process for modifying the production of carotenoids in a plant, ~~either by increasing the production of carotenoids, or by reducing or inhibiting the production of carotenoids by the plant,~~ relative to the normal content of carotenoids produced by the plant,

\_\_\_\_\_ said process comprising ~~the transformation of cells of said plants to be transformed with a vector according to Claim 10~~ adapted to increase carotenoid biosynthesis, said vector comprising all or a portion of the nucleotide sequence SEQ ID NO: 1, encoding all or a portion of an enzyme involved in carotenoid synthesis, represented by SEQ ID NO: 2, preceded by a promotor, such that the vector can generate mRNA in the plant cells,  
\_\_\_\_\_ wherein production of carotenoids in said plant is increased.

15. (Currently Amended) Process for producing carotenoids in a plant cell, or eukaryotic or prokaryotic cell,  
\_\_\_\_\_ said process comprising ~~the transformation of cells of said plants~~ at least one plant, eukaryotic or prokaryotic cells to be transformed with a vector according to Claim 10 adapted to increase carotenoid biosynthesis, said vector comprising all or a portion of the nucleotide sequence SEQ ID NO: 1, encoding all or a portion of an enzyme involved in carotenoid synthesis, represented by SEQ ID NO: 2, preceded by a promotor, such that the vector can generate mRNA in said at least one cell,  
\_\_\_\_\_ wherein production of carotenoids in said plant, eukaryotic or prokaryotic cell is increased.

16-19. (Canceled)

20. (New) The process according to claim 14, wherein said vector comprises a nucleotide sequence encoding SEQ ID NO: 2.
21. (New) The process according to claim 14, wherein said vector comprises a nucleotide sequence having at least 70% homology with the coding region of SEQ ID NO: 1, said coding region being at nucleotides 130 to 1182 of SEQ ID NO: 1.
22. (New) The process according to claim 21, wherein said vector comprises a nucleotide sequence having at least 80% homology with said coding region of SEQ ID NO: 1.
23. (New) The process according to claim 21, wherein said vector comprises a nucleotide sequence having at least 90% homology with said coding region of SEQ ID NO: 1.
24. (New) The process according to claim 21, wherein said vector comprises a nucleotide sequence having at least 95% homology with said coding region of SEQ ID NO: 1.
25. (New) The process according to claim 15, wherein said vector comprises a nucleotide sequence encoding SEQ ID NO: 2.
26. (New) The process according to claim 15, wherein said vector comprises a nucleotide sequence having at least 70% homology with the coding region of SEQ ID NO: 1, said coding region being at nucleotides 130 to 1182 of SEQ ID NO: 1.
27. (New) The process according to claim 26, wherein said vector comprises a nucleotide sequence having at least 80% homology with said coding region of SEQ ID NO: 1.
28. (New) The process according to claim 26, wherein said vector comprises a nucleotide sequence having at least 90% homology with said coding region of SEQ ID NO: 1.
29. (New) The process according to claim 26, wherein said vector comprises a nucleotide sequence having at least 95% homology with said coding region of SEQ ID NO: 1.